

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Freeman, Gordon J.
Nadler, Lee M.
Gray, Gary S.

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(ii) TITLE OF INVENTION: Novel CTLA4/CD28 Ligands and
Uses Therefor

(iii) NUMBER OF SEQUENCES: 31

15

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/280,757; 08/101,624; 08/109,393;
08/147,773
(B) FILING DATE: 26-JUL-1994; 26-JUL-1993; 19-AUG-1993; 03-NOV-
1993

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(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: RPI-004CP3

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 107..1093

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
20	GAGTGGGGTC ATTTCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC	115
	Met Asp Pro	
	1	
25	CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG	163
	Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu	
	5 10 15	
30	CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT	211
	Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr	
	20 25 30 35	
35	GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT	259
	Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser	
	40 45 50	
40	GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG	307
	Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu	
	55 60 65	
45	GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG	355
	Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	
	70 75 80	
50	GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403
	Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	
	85 90 95	
55	CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA	451
	Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	
	100 105 110 115	
	AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA	499
	Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	
	120 125 130	

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	GTG	CTT	GCT	AAC	TTC	AGT	CAA	CCT	GAA	ATA	GTA	CCA	ATT	TCT	AAT	ATA	547
	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Asn	Ile	
				135					140					145			
5	ACA	GAA	AAT	GTG	TAC	ATA	AAT	TTG	ACC	TGC	TCA	TCT	ATA	CAC	GGT	TAC	595
	Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	His	Gly	Tyr	
			150					155					160				
10	CCA	GAA	CCT	AAG	AAG	ATG	AGT	GTT	TTG	CTA	AGA	ACC	AAG	AAT	TCA	ACT	643
	Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	
		165					170					175					
15	ATC	GAG	TAT	GAT	GGT	ATT	ATG	CAG	AAA	TCT	CAA	GAT	AAT	GTC	ACA	GAA	691
	Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	
	180					185					190					195	
20	CTG	TAC	GAC	GTT	TCC	ATC	AGC	TTG	TCT	GTT	TCA	TTC	CCT	GAT	GTT	ACG	739
	Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	
					200					205					210		
	AGC	AAT	ATG	ACC	ATC	TTC	TGT	ATT	CTG	GAA	ACT	GAC	AAG	ACG	CGG	CTT	787
	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	
				215					220					225			
25	TTA	TCT	TCA	CCT	TTC	TCT	ATA	GAG	CTT	GAG	GAC	CCT	CAG	CCT	CCC	CCA	835
	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	
			230					235					240				
30	GAC	CAC	ATT	CCT	TGG	ATT	ACA	GCT	GTA	CTT	CCA	ACA	GTT	ATT	ATA	TGT	883
	Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	
		245					250					255					
35	GTG	ATG	GTT	TTC	TGT	CTA	ATT	CTA	TGG	AAA	TGG	AAG	AAG	AAG	AAG	CGG	931
	Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg	
	260					265					270					275	
40	CCT	CGC	AAC	TCT	TAT	AAA	TGT	GGA	ACC	AAC	ACA	ATG	GAG	AGG	GAA	GAG	979
	Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	
					280					285					290		
	AGT	GAA	CAG	ACC	AAG	AAA	AGA	GAA	AAA	ATC	CAT	ATA	CCT	GAA	AGA	TCT	1027
	Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	
				295					300					305			
45	GAT	GAA	GCC	CAG	CGT	GTT	TTT	AAA	AGT	TCG	AAG	ACA	TCT	TCA	TGC	GAC	1075
	Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp	
			310					315					320				
50	AAA	AGT	GAT	ACA	TGT	TTT	TAATTAAAGA	GTAAAGCCCA	AAAAAAA								1120
	Lys	Ser	Asp	Thr	Cys	Phe											
			325														

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Pro	Gln	Cys	Thr	Met	Gly	Leu	Ser	Asn	Ile	Leu	Phe	Val	Met	1	5	10	15
Ala	Phe	Leu	Leu	Ser	Gly	Ala	Ala	Pro	Leu	Lys	Ile	Gln	Ala	Tyr	Phe	20	25	30	
Asn	Glu	Thr	Ala	Asp	Leu	Pro	Cys	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln	35	40	45	
Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val	50	55	60	
Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His	Ser	65	70	75	80
Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg	85	90	95	
Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	100	105	110	
His	His	Lys	Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	115	120	125	
Glu	Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	130	135	140	
Ser	Asn	Ile	Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	145	150	155	160
His	Gly	Tyr	Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	165	170	175	
Asn	Ser	Thr	Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	180	185	190	
Val	Thr	Glu	Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	195	200	205	
Asp	Val	Thr	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	210	215	220	
Thr	Arg	Leu	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	225	230	235	240

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Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
 245 250 255

5 Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
 260 265 270

Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
 275 280 285

10 Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
 290 295 300

15 Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
 305 310 315 320

Ser Cys Asp Lys Ser Asp Thr Cys Phe
 325

20 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAATACGACT CACTATAGGG 20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAAGGTTCCCT TCACAAAG 18

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: oligonucleotide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTGGTAGGT ATGGAAGATC C

21

(2) INFORMATION FOR SEQ ID NO:6:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: oligonucleotide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCGAATCA TTCCTGTGGG C

21

(2) INFORMATION FOR SEQ ID NO:7:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: oligonucleotide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAGCCCACA GGAATGATTC G

21

45 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: oligonucleotide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCTCAAAAC CAAAGCCTGA G

21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTAGGTCACA GCAGAAGCAG C

21

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCTGGAAACT GACAAGACGC G

21

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTCAGGCTTT GGTTTTGAGA G

21

662207 "9752460

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTCTCTTC CCTCTCCATT G 21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACAAGCTGA TGGAAACGTC G 21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAATGGAGAG GGAAGAGAGT G 21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: oligonucleotide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTTTAGAGCA CA

12

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTCTAAAG

8

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

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(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Tyr Met Gly Arg Thr Ser Phe Asp

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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002201 91552160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Ser Gln Asp Asn Val Thr Glu Lys Tyr Asp Val Ser
5 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys
20 5 10 15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGCCCATGG CTTCAGA

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCCAAAATGG ATCCCCA

17

17

00552201 " 91532460

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 111..1040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

20	CCCACGCGTC CGGGAGCAAG CAGACGCGTA AGAGTGGCTC CTGTAGGCAG CACGGACTTG	60
	AACAACCAGA CTCCTGTAGA CGTGTTCAG AACTTACGGA AGCACCCACG ATG GAC	116
		Met Asp
		1
25	CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG	164
	Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu	
	5 10 15	
30	CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG	212
	Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly	
	20 25 30	
35	ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG	260
	Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu	
	35 40 45 50	
40	AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC	308
	Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr	
	55 60 65	
	GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC	356
	Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr	
	70 75 80	
45	CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC	404
	Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His	
	85 90 95	
50	AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA	452
	Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys	
	100 105 110	
55	AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG	500
	Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu	
	115 120 125 130	

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	TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT	548
	Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn	
	135 140 145	
5	GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT	596
	Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly	
	150 155 160	
10	CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT	644
	His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn	
	165 170 175	
15	GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG	692
	Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu	
	180 185 190	
20	TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG	740
	Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp	
	195 200 205 210	
25	CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC	788
	His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser	
	215 220 225	
30	TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT	836
	Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr	
	230 235 240	
35	TGG AAG GAG ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG	884
	Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met	
	245 250 255	
40	CTG CTC ATC ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC	932
	Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro	
	260 265 270	
45	AGC AAC ACA GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG	980
	Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu	
	275 280 285 290	
50	ACT ATC AAC CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA	1028
	Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro	
	295 300 305	
55	AAT GCA GAG TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT	1077
	Asn Ala Glu	
60	TTGCCTGAAA TAAGAAGTGC AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA	1137
	ATTCTACAGT TGAATAATTA AAGAAC	1163

65220T" 9T552460

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Asp Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr
1 5 10 15
Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe
20 25 30
Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile
35 40 45
Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val
50 55 60
Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala
25 65 70 75 80
Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg
85 90 95
Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile
30 100 105 110
Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr
115 120 125
Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala
35 130 135 140
Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys
40 145 150 155 160
Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser
165 170 175
Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr
45 180 185 190
Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly
195 200 205
Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys
50 210 215 220
Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln
55 225 230 235 240

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Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu
245 250 255

5 Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser
260 265 270

Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp
275 280 285

10 Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala
290 295 300

Lys Pro Asn Ala Glu
15 305

(2) INFORMATION FOR SEQ ID NO:24:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: oligonucleotide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACATAAGCCT GAGTGAGCTG G

21

35 (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGATGAGCA GCATCACAAG G

50

21

005516 101 97552460

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

15 TGGTCGAGTG AGTCCGAATA C

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

30 GACGAGTAGT AACATACAGT G

21

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

662207 "9TSGA60

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: Homo sapien
(F) TISSUE TYPE: lymphoid
(G) CELL TYPE: B cell
(H) CELL LINE: Raji

(vii) IMMEDIATE SOURCE:

- 10 (A) LIBRARY: cDNA in pCDM8 vector
(B) CLONE: B7, Raji clone #13

(viii) POSITION IN GENOME:

- 15 (A) CHROMOSOME/SEGMENT: 3

(ix) FEATURE:

- 20 (A) NAME/KEY: Open reading frame (translated region)
(B) LOCATION: 318 to 1181 bp
(C) IDENTIFICATION METHOD: similarity to other pattern

(ix) FEATURE:

- 25 (A) NAME/KEY: Alternate polyadenylation signal
(B) LOCATION: 1474 to 1479 bp
(C) IDENTIFICATION METHOD: similarity to other pattern

(x) PUBLICATION INFORMATION:

- 30 (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
35 WHITMAN, JAMES F.
NADLER, LEE M.

(B) TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
40
(C) JOURNAL: The Journal of Immunology
(D) VOLUME: 143
(E) ISSUE: 8
(F) PAGES: 2714-2722
45 (G) DATE: 15-OCT-1989
(H) RELEVANT RESIDUES In SEQ ID NO:28: FROM 1 TO 1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

50 CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60
GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCT TCAAGCAAGCT 120
55 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180

GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240
 TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGGGCTTT CACTTTTGAC 300
 5 CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 353
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
 -30 -25

10 AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 401
 Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
 -20 -15 -10

15 TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 449
 Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
 -5 1 5 10

20 GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA 497
 Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala
 15 20 25

25 CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG 545
 Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met
 30 35 40

30 ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC 593
 Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile
 45 50 55

35 TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA 641
 Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro
 60 65 70

40 TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC 689
 Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp
 75 80 85 90

45 GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT 737
 Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala
 95 100 105

50 GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT 785
 Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn
 110 115 120

55

66220T" 9T55C460

	ATT	AGA	AGG	ATA	ATT	TGC	TCA	ACC	TCT	GGA	GGT	TTT	CCA	GAG	CCT	CAC	833
	Ile	Arg	Arg	Ile	Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	
			125					130					135				
5	CTC	TCC	TGG	TTG	GAA	AAT	GGA	GAA	GAA	TTA	AAT	GCC	ATC	AAC	ACA	ACA	881
	Leu	Ser	Trp	Leu	Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	
			140				145					150					
10	GTT	TCC	CAA	GAT	CCT	GAA	ACT	GAG	CTC	TAT	GCT	GTT	AGC	AGC	AAA	CTG	929
	Val	Ser	Gln	Asp	Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu	
	155					160				165						170	
15	GAT	TTC	AAT	ATG	ACA	ACC	AAC	CAC	AGC	TTC	ATG	TGT	CTC	ATC	AAG	TAT	977
	Asp	Phe	Asn	Met	Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr	
					175					180					185		
20	GGA	CAT	TTA	AGA	GTG	AAT	CAG	ACC	TTC	AAC	TGG	AAT	ACA	ACC	AAG	CAA	1025
	Gly	His	Leu	Arg	Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln	
				190					195					200			
25	GAG	CAT	TTT	CCT	GAT	AAC	CTG	CTC	CCA	TCC	TGG	GCC	ATT	ACC	TTA	ATC	1073
	Glu	His	Phe	Pro	Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	Ile	
			205				210					215					
30	TCA	GTA	AAT	GGA	ATT	TTT	GTG	ATA	TGC	TGC	CTG	ACC	TAC	TGC	TTT	GCC	1121
	Ser	Val	Asn	Gly	Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe	Ala	
		220					225					230					
35	CCA	AGA	TGC	AGA	GAG	AGA	AGG	AGG	AAT	GAG	AGA	TTG	AGA	AGG	GAA	AGT	1169
	Pro	Arg	Cys	Arg	Glu	Arg	Arg	Arg	Asn	Glu	Arg	Leu	Arg	Arg	Glu	Ser	
	235					240				245					250		
40	GTA	CGC	CCT	GTA	TAACAGT	GTGTC	CGCAGAAGCA	AGGGGCTGAA	AAGATCTGAA								1221
	Val	Arg	Pro	Val													
45	GGTAGCCTCC	GTCATCTCTT	CTGGGATA	TAC	TGGATCGTGG	GGATCATGAG	GCATTCTTCC										1281
	CTTAACAAAT	TTAAGCTGTT	TTACCCACTA	CCTCACCTTC	TTAAAAACCT	CTTTCAGATT											1341
50	AAGCTGAACA	GTTACAAGAT	GGCTGGCATC	CCTCTCCTTT	CTCCCCATAT	GCAATTTGCT											1401
	TAATGTAACC	TCTTCTTTTG	CCATGTTTCC	ATTCTGCCAT	CTTGAATTGT	CTTGTCAGCC											1461
55																	

662220T" 9T552466

AATTCATTAT CTATTAAACA CTAATTTGAG
1491

5

(3) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein

20

(ix) FEATURE:

- (A) NAME/KEY: signal sequence
- (B) LOCATION: -34 to -1
- (C) IDENTIFICATION METHOD: amino terminal sequencing of
soluble protein
- (D) OTHER INFORMATION: hydrophobic

25

(ix) FEATURE:

- (A) NAME/KEY: extracellular domain
- (B) LOCATION: 1 to 208
- (C) IDENTIFICATION METHOD: similarity with known
sequence

30

35

(ix) FEATURE:

- (A) NAME/KEY: transmembrane domain
- (B) LOCATION: 209 to 235
- (C) IDENTIFICATION METHOD: similarity with known
sequence

40

(ix) FEATURE:

- (A) NAME/KEY: intracellular domain
- (B) LOCATION: 236 to 254
- (C) IDENTIFICATION METHOD: similarity with known
sequence

45

50

094551610699

(ix) FEATURE:

- 5 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 19 to 21
(C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- 10 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 55 to 57
(C) IDENTIFICATION METHOD: similarity with known sequence

15

(ix) FEATURE:

- 20 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 64 to 66
(C) IDENTIFICATION METHOD: similarity with known sequence

25 (ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 152 to 154
(C) IDENTIFICATION METHOD: similarity with known sequence

30

(ix) FEATURE:

- 35 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 173 to 175
(C) IDENTIFICATION METHOD: similarity with known sequence

40

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 177 to 179
(C) IDENTIFICATION METHOD: similarity with known sequence

45

(ix) FEATURE:

- 50 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 192 to 194
(C) IDENTIFICATION METHOD: similarity with known sequence

55

044551-1090

5 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 198 to 200
(C) IDENTIFICATION METHOD: similarity with known sequence

15 (A) NAME/KEY: Ig V-set domain
(B) LOCATION: 1 to 104
(C) IDENTIFICATION METHOD: similarity with known sequence

20 (A) NAME/KEY: Ig C-set domain
(B) LOCATION: 105 to 202
(C) IDENTIFICATION METHOD: similarity with known sequence

30 (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
NADLER, LEE M.

35 (B) TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
(C) JOURNAL: The Journal of Immunology
(D) VOLUME: 143
(E) ISSUE: 8
(F) PAGES: 2714-2722
40 (G) DATE: 15-OCT-1989
(H) RELEVANT RESIDUES IN SEQUENCE ID NO:29: From -26 to 262

45

	Met	Gly	His	Thr	Arg	Arg	Gln	Gly	Thr	Ser	Pro	Ser	Lys	Cys	Pro	Tyr	
					-30					-25					-20		
5	Leu	Asn	Phe	Phe	Gln	Leu	Leu	Val	Leu	Ala	Gly	Leu	Ser	His	Phe	Cys	
				-15					-10					-5			
	Ser	Gly	Val	Ile	His	Val	Thr	Lys	Glu	Val	Lys	Glu	Val	Ala	Thr	Leu	
	-1		1					5				10					
10	Ser	Cys	Gly	His	Asn	Val	Ser	Val	Glu	Glu	Leu	Ala	Gln	Thr	Arg	Ile	
	15					20					25					30	
	Tyr	Trp	Gln	Lys	Glu	Lys	Lys	Met	Val	Leu	Thr	Met	Met	Ser	Gly	Asp	
					35					40					45		
15	Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Ile	Phe	Asp	Ile	Thr	
				50					55					60			
	Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	Pro	Ser	Asp	Glu	Gly	
20			65					70					75				
	Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	Asp	Ala	Phe	Lys	Arg	
	80						85					90					
25	Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	Ala	Asp	Phe	Pro	Thr	
	95					100					105					110	
	Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	Asn	Ile	Arg	Arg	Ile	
					115					120					125		
30	Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	Leu	Ser	Trp	Leu	
				130					135					140			
	Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	Val	Ser	Gln	Asp	
35			145					150					155				
	Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu	Asp	Phe	Asn	Met	
		160					165					170					
40	Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr	Gly	His	Leu	Arg	
	175					180					185					190	
	Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln	Glu	His	Phe	Pro	
45					195					200					205		
	Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	Ile	Ser	Val	Asn	Gly	
			210						215					220			
50	Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe	Ala	Pro	Arg	Cys	Arg	
		225						230					235				
	Glu	Arg	Arg	Arg	Asn	Glu	Arg	Leu	Arg	Arg	Glu	Ser	Val	Arg	Pro	Val	
		240					245					250					
55																	

004554 1033

(4) INFORMATION FOR SEQ ID NO:30:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(ii) MOLECULAR TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus
- (D) DEVELOPMENTAL STAGE: germ line
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B lymphocyte
- (H) CELL LINE: 70Z and A20

20

(vii) IMMEDIATE SOURCE:

25

- (A) LIBRARY: cDNA in pCDM8 vector
- (B) CLONE: B7 #'s 1 and 29

(ix) FEATURE:

30

- (A) NAME/KEY: translated region
- (B) LOCATION: 249 to 1166 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

(ix) FEATURE:

35

- (A) NAME/KEY: Alternate ATG initiation codons
- (B) LOCATION: 225 to 227 and 270 to 272
- (C) IDENTIFICATION METHOD: similarity to other pattern

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

045541039
662201"9T552460

GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
 5 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180
 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240
 10 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 -35 -30 -25
 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
 15 Lys Phe Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg
 -20 -15 -10
 CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG 386
 Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
 -5 -1 1 5
 20 AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT 434
 Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
 10 15 20 25
 25 GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG 482
 Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
 30 35 40
 30 TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG 530
 Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
 45 50 55
 35 ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC 578
 Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
 60 65 70
 CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA 626
 Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
 75 80 85
 40 GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA 674
 Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys
 90 95 100 105
 45 GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA 722
 Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala
 110 115 120
 50 GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT 770
 Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro
 125 130 135
 55 CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG 818
 Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr
 140 145 150

0045516 102259

[illegible]

(5) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 10 (A) DESCRIPTION: B lymphocyte activation antigen; Ig
superfamily member; T cell costimulatory signal
via activation of CD28 pathways, binds to CD28⁺
T cells, transmembrane protein

15 (ix) FEATURE:

- (A) NAME/KEY: signal sequence
(B) LOCATION: -37 to -1
20 (C) IDENTIFICATION METHOD: similarity with known
sequence
(D) OTHER INFORMATION: hydrophobic

25 (ix) FEATURE:

- (A) NAME/KEY: extracellular domain
(B) LOCATION: 1 to 210
30 (C) IDENTIFICATION METHOD: similarity with known
sequence

(ix) FEATURE:

- 35 (A) NAME/KEY: transmembrane domain
(B) LOCATION: 211 to 235
(C) IDENTIFICATION METHOD: similarity with known
sequence

40 (ix) FEATURE:

- (A) NAME/KEY: intracellular (cytoplasmic) domain
(B) LOCATION: 236 to 269
45 (C) IDENTIFICATION METHOD: similarity with known
sequence

(ix) FEATURE:

- 50 (A) NAME/KEY: Ig V-set domain
(B) LOCATION: 1 to 105
(C) IDENTIFICATION METHOD: similarity with known
sequence

55

65201" 9153460

(ix) FEATURE:

- (A) NAME/KEY: Ig C-set domain
 (B) LOCATION: 106 to 199
 5 (C) IDENTIFICATION METHOD: similarity with known sequence

(x) PUBLICATION INFORMATION:

- 10 (A) AUTHORS: FREEMAN, GORDON J.
 GRAY, GARY S.
 GIMMI, CLAUDE D.
 LOMBARD, DAVID B.
 15 ZHOU, LIANG-JI
 WHITE, MICHAEL
 FINGEROTH, JOYCE D.
 GRIBBEN, JOHN G.
 NADLER, LEE M.
 20 (B) TITLE: Structure, Expression, and T Cell Costimulatory
 Activity Of The Murine Homologue Of The Human B
 Lymphocyte Activation Antigen B7
 (C) JOURNAL: Journal of Experimental Medicine
 25 (D) VOLUME:
 (E) ISSUE:
 (F) PAGES:
 (G) DATE: IN PRESS
 (H) RELEVANT RESIDUES IN SEQUENCE ID NO:31: From -37 to 269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

35 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 -35 -30 -25
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 -20 -15 -10
 40 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
 -5 -1 1 5 10
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
 45 15 20 25
 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 30 35 40
 50 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
 45 50 55
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
 60 65 70 75

55

045516 " 9152460

-118-

	Asp	Arg	Gly	Thr	Tyr	Ser	Cys	Val	Val	Gln	Lys	Lys	Glu	Arg	Gly	Thr	
						80					85					90	
5	Tyr	Gly	Val	Lys	His	Leu	Ala	Leu	Val	Lys	Leu	Ser	Ile	Lys	Ala	Asp	
				95					100					105			
	Phe	Ser	Thr	Pro	Asn	Ile	Thr	Glu	Ser	Gly	Asn	Pro	Ser	Ala	Asp	Thr	
			110					115					120				
10	Lys	Arg	Ile	Thr	Cys	Phe	Ala	Ser	Gly	Gly	Phe	Pro	Lys	Pro	Arg	Phe	
		125					130					135					
	Ser	Trp	Leu	Glu	Asn	Gly	Arg	Glu	Leu	Pro	Gly	Ile	Asn	Thr	Thr	Ile	
	140					145					150					155	
15	Ser	Gln	Asp	Pro	Glu	Ser	Glu	Leu	Tyr	Thr	Ile	Ser	Ser	Gln	Leu	Asp	
				160						165					170		
	Phe	Asn	Thr	Thr	Arg	Asn	His	Thr	Ile	Lys	Cys	Leu	Ile	Lys	Tyr	Gly	
20				175					180					185			
	Asp	Ala	His	Val	Ser	Glu	Asp	Phe	Thr	Trp	Glu	Lys	Pro	Pro	Glu	Asp	
			190					195					200				
25	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	Val	Leu	Phe	Gly	Ala	Gly	Phe	Gly	
		205					210					215					
	Ala	Val	Ile	Thr	Val	Val	Val	Ile	Val	Val	Ile	Ile	Lys	Cys	Phe	Cys	
	220					225					230					235	
30	Lys	His	Arg	Ser	Cys	Phe	Arg	Arg	Asn	Glu	Ala	Ser	Arg	Glu	Thr	Asn	
					240					245					250		
	Asn	Ser	Leu	Thr	Phe	Gly	Pro	Glu	Glu	Ala	Leu	Ala	Glu	Gln	Thr	Val	
35				255					260					265			
	Phe	Leu															

40

004255 1022460